SEQUENCE LISTING

<110> Schimmel, Paul
Wakasugi, Keisuke
Friedlander, Martin

<120> Tryptophanyl-tRNA Synthetase Derived
Polypeptides Useful For The Regulation of Angiogenesis

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<150> 60/270,951
<151> 2001-02-23

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Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro
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Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser
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Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile
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Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe
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Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile
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Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys
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Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg
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Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg
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Thr Glu Ala Glu Glu Asp Phe Val Asp Pro Trp Thr Val Gln Thr Ser
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agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg ttt gga agt   3613
Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser
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agt aaa att gac aaa gag cta ata aac cga ata gag aga gcc acc ggc   3661
Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly
         65                  70                  75

caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc tca cac aga   3709
Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg
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gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag cca ttt tat   3757
Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr
 95                 100                 105                 110

ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat gta ggt cac   3805
Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His
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ctc att cca ttt att ttc aca aag tgg ctc cag gat gta ttt aac gtg   3853
Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val
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ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg tgg aag gac   3901
Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp
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ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat gcc aag gac   3949
Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp
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atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata ttc tct gac   3997
Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp
175                 180                 185                 190

ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat gtg gtg aag   4045
Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys
                195                 200                 205

att caa aag cat gtt acc ttc aac caa gtg aaa ggc att ttc ggc ttc   4093
Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe
            210                 215                 220

act gac agc gac tgc att ggg aag atc agt ttt cct gcc atc cag gct   4141
Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala
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gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga gac agg acg   4189
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gat atc cag tgc ctt atc cca tgt gcc att gac cag gat cct tac ttt   4237
Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
255                 260                 265                 270

aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct aaa cca gcc   4285
Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala
                275                 280                 285

ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc cag acc aaa   4333
Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys
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atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc gac acg gcc   4381
Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala
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aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct gga ggg aga   4429
Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg
    320                 325                 330

gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt gat gtg gac   4477
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gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac gac aag ctc   4525
Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu
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gag cag atc agg aag gat tac acc agc gga gcc atg ctc acc ggt gag   4573
Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu
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ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc gca gag cac   4621
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cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa gag ttc atg   4669
Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met
    400                 405                 410

act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg gcc gca ctc   4717
Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu
415                 420                 425                 430

gag cac cac cac cac cac cac tgagatccgg ctgctaacaa agcccgaaag      4768
Glu His His His His His His
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        35                  40                  45
Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys
    50                  55                  60
Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg
65                  70                  75                  80
Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met
                85                  90                  95
Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr
            100                 105                 110
Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile
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Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu
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Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr
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Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile
                165                 170                 175
Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp
            180                 185                 190
Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln
        195                 200                 205
Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp
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Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro
225                 230                 235                 240
Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile
                245                 250                 255
Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met
            260                 265                 270
Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu
        275                 280                 285
His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser
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Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln
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Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala
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Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro
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tatacat atg agt aat cat ggc cca gat gcc aca gaa gct gaa gag gat   3469
        Met Ser Asn His Gly Pro Asp Ala Thr Glu Ala Glu Glu Asp
         1               5                  10

ttt gtg gac cca tgg aca gta cag aca agc agt gca aaa ggc ata gac   3517
Phe Val Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp
 15                  20                  25                  30

tac gat aag ctc att gtt cgg ttt gga agt agt aaa att gac aaa gag   3565
Tyr Asp Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu
                 35                  40                  45

cta ata aac cga ata gag aga gcc acc ggc caa aga cca cac cac ttc   3613
Leu Ile Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe
             50                  55                  60

ctg cgc aga ggc atc ttc ttc tca cac aga gat atg aat cag gtt ctt   3661
Leu Arg Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu
         65                  70                  75

gat gcc tat gaa aat aag aag cca ttt tat ctg tac acg ggc cgg ggc   3709
Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly
     80                  85                  90

ccc tct tct gaa gca atg cat gta ggt cac ctc att cca ttt att ttc   3757
Pro Ser Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe
 95                  100                 105                 110
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aca aag tgg ctc cag gat gta ttt aac gtg ccc ttg gtc atc cag atg   3805
Thr Lys Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met
                115                 120                 125

acg gat gac gag aag tat ctg tgg aag gac ctg acc ctg gac cag gcc   3853
Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala
            130                 135                 140

tat ggc gat gct gtt gag aat gcc aag gac atc atc gcc tgt ggc ttt   3901
Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe
        145                 150                 155

gac atc aac aag act ttc ata ttc tct gac ctg gac tac atg ggg atg   3949
Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met
    160                 165                 170

agc tca ggt ttc tac aaa aat gtg gtg aag att caa aag cat gtt acc   3997
Ser Ser Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr
175                 180                 185                 190

ttc aac caa gtg aaa ggc att ttc ggc ttc act gac agc gac tgc att   4045
Phe Asn Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile
                195                 200                 205

ggg aag atc agt ttt cct gcc atc cag gct gct ccc tcc ttc agc aac   4093
Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn
            210                 215                 220

tca ttc cca cag atc ttc cga gac agg acg gat atc cag tgc ctt atc   4141
Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile
        225                 230                 235

cca tgt gcc att gac cag gat cct tac ttt aga atg aca agg gac gtc   4189
Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val
    240                 245                 250

gcc ccc agg atc ggc tat cct aaa cca gcc ctg ttg cac tcc acc ttc   4237
Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe
255                 260                 265                 270

ttc cca gcc ctg cag ggc gcc cag acc aaa atg agt gcc agc gac cca   4285
Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro
                275                 280                 285

aac tcc tcc atc ttc ctc acc gac acg gcc aag cag atc aaa acc aag   4333
Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys
            290                 295                 300

gtc aat aag cat gcg ttt tct gga ggg aga gac acc atc gag gag cac   4381
Val Asn Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His
        305                 310                 315

agg cag ttt ggg ggc aac tgt gat gtg gac gtg tct ttc atg tac ctg   4429
Arg Gln Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu
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    320                 325                 330

acc ttc ttc ctc gag gac gac gac aag ctc gag cag atc agg aag gat   4477
Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp
335                 340                 345                 350

tac acc agc gga gcc atg ctc acc ggt gag ctc aag aag gca ctc ata   4525
Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile
                355                 360                 365

gag gtt ctg cag ccc ttg atc gca gag cac cag gcc cgg cgc aag gag   4573
Glu Val Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu
            370                 375                 380

gtc acg gat gag ata gtg aaa gag ttc atg act ccc cgg aag ctg tcc   4621
Val Thr Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser
        385                 390                 395

ttc gac ttt cag aag ctt gcg gcc gca ctc gag cac cac cac cac cac   4669
Phe Asp Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His
    400                 405                 410

cac tgagatccgg ctgctaacaa agcccgaaag gaagctgagt tggctgctgc        4722
His
415

caccgctgag caataactag cataacccct tggggcctct aaacgggtct tgaggggttt 4782
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<213> Artificial Sequence

<220>
<223> Cleavage Product T1 of recombinant human TrpRS

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Asp Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp Tyr Asp
            20                  25                  30
Lys Leu Ile Val Arg Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile
        35                  40                  45
Asn Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg
    50                  55                  60
Arg Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala
65                  70                  75                  80
Tyr Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser
                85                  90                  95
Ser Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys
            100                 105                 110
Trp Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp
        115                 120                 125
Asp Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly
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    130                 135                 140
Asp Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile
145                 150                 155                 160
Asn Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser
                165                 170                 175
Gly Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn
            180                 185                 190
Gln Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys
        195                 200                 205
Ile Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe
    210                 215                 220
Pro Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys
225                 230                 235                 240
Ala Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro
                245                 250                 255
Arg Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro
            260                 265                 270
Ala Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser
        275                 280                 285
Ser Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn
    290                 295                 300
Lys His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln
305                 310                 315                 320
Phe Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe
                325                 330                 335
Phe Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr
            340                 345                 350
Ser Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val
        355                 360                 365
Leu Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr
    370                 375                 380
Asp Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp
385                 390                 395                 400
Phe Gln Lys Leu Ala Ala Ala Leu Glu His His His His His His
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<210> 6
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<220>
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<221> CDS
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acgtagtggg ccatcgccct gatagacggt ttttcgccct ttgacgttgg agtccacgtt 300
ctttaatagt ggactcttgt tccaaactgg aacaacactc aaccctatct cggtctattc 360

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tatagggaga ccacaacggt ttccctctag aaataatttt gtttaacttt aagaaggaga 3420
tatacat atg agt gca aaa ggc ata gac tac gat aag ctc att gtt cgg 3469
Met Ser Ala Lys Gly Ile Asp Tyr Asp Lys Leu Ile Val Arg
1 5 10

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ttt gga agt agt aaa att gac aaa gag cta ata aac cga ata gag aga   3517
Phe Gly Ser Ser Lys Ile Asp Lys Glu Leu Ile Asn Arg Ile Glu Arg
 15                  20                  25                  30

gcc acc ggc caa aga cca cac cac ttc ctg cgc aga ggc atc ttc ttc   3565
Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe
                 35                  40                  45

tca cac aga gat atg aat cag gtt ctt gat gcc tat gaa aat aag aag   3613
Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys
             50                  55                  60

cca ttt tat ctg tac acg ggc cgg ggc ccc tct tct gaa gca atg cat   3661
Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His
         65                  70                  75

gta ggt cac ctc att cca ttt att ttc aca aag tgg ctc cag gat gta   3709
Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val
     80                  85                  90

ttt aac gtg ccc ttg gtc atc cag atg acg gat gac gag aag tat ctg   3757
Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu
 95                  100                 105                 110

tgg aag gac ctg acc ctg gac cag gcc tat ggc gat gct gtt gag aat   3805
Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn
                115                 120                 125

gcc aag gac atc atc gcc tgt ggc ttt gac atc aac aag act ttc ata   3853
Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile
            130                 135                 140

ttc tct gac ctg gac tac atg ggg atg agc tca ggt ttc tac aaa aat   3901
Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn
        145                 150                 155

gtg gtg aag att caa aag cat gtt acc ttc aac caa gtg aaa ggc att   3949
Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile
    160                 165                 170

ttc ggc ttc act gac agc gac tgc att ggg aag atc agt ttt cct gcc   3997
Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala
175                 180                 185                 190

atc cag gct gct ccc tcc ttc agc aac tca ttc cca cag atc ttc cga   4045
Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg
                195                 200                 205

gac agg acg gat atc cag tgc ctt atc cca tgt gcc att gac cag gat   4093
Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp
            210                 215                 220

cct tac ttt aga atg aca agg gac gtc gcc ccc agg atc ggc tat cct   4141
Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro
        225                 230                 235
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aaa cca gcc ctg ttg cac tcc acc ttc ttc cca gcc ctg cag ggc gcc   4189
Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala
    240                 245                 250

cag acc aaa atg agt gcc agc gac cca aac tcc tcc atc ttc ctc acc   4237
Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr
255                 260                 265                 270

gac acg gcc aag cag atc aaa acc aag gtc aat aag cat gcg ttt tct   4285
Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser
                275                 280                 285

gga ggg aga gac acc atc gag gag cac agg cag ttt ggg ggc aac tgt   4333
Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys
            290                 295                 300

gat gtg gac gtg tct ttc atg tac ctg acc ttc ttc ctc gag gac gac   4381
Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp
        305                 310                 315

gac aag ctc gag cag atc agg aag gat tac acc agc gga gcc atg ctc   4429
Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu
    320                 325                 330

acc ggt gag ctc aag aag gca ctc ata gag gtt ctg cag ccc ttg atc   4477
Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile
335                 340                 345                 350

gca gag cac cag gcc cgg cgc aag gag gtc acg gat gag ata gtg aaa   4525
Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys
                355                 360                 365

gag ttc atg act ccc cgg aag ctg tcc ttc gac ttt cag aag ctt gcg   4573
Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala
            370                 375                 380

gcc gca ctc gag cac cac cac cac cac cac tgagatccgg ctgctaacaa     4623
Ala Ala Leu Glu His His His His His His
        385                 390

agcccgaaag gaagctgagt tggctgctgc caccgctgag caataactag cataacccct 4683
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<220>
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            20                  25                  30
Gly Gln Arg Pro His His Phe Leu Arg Arg Gly Ile Phe Phe Ser His
        35                  40                  45
Arg Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe
    50                  55                  60
Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly
65                  70                  75                  80
His Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn
                85                  90                  95
Val Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys
            100                 105                 110
Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys
        115                 120                 125
Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser
    130                 135                 140
Asp Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val
145                 150                 155                 160
Lys Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly
                165                 170                 175
Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln
            180                 185                 190
Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg
        195                 200                 205
Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr
    210                 215                 220
Phe Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro
225                 230                 235                 240
Ala Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr
                245                 250                 255
Lys Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr
            260                 265                 270
Ala Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly
        275                 280                 285
Arg Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val
    290                 295                 300
Asp Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys
305                 310                 315                 320
Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly
                325                 330                 335
Glu Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu
            340                 345                 350
His Gln Ala Arg Arg Lys Glu Val Thr Asp Glu Ile Val Lys Glu Phe
        355                 360                 365
Met Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln Lys Leu Ala Ala Ala
    370                 375                 380
Leu Glu His His His His His His
385                 390
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<210> 8
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<212> PRT
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<400> 8
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1 5

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Lys Met Ser Ala Ser
1 5

<210> 12
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35 40 45
Asp Met Asn Gln Val Leu Asp Ala Tyr Glu Asn Lys Lys Pro Phe Tyr
50 55 60
Leu Tyr Thr Gly Arg Gly Pro Ser Ser Glu Ala Met His Val Gly His
65 70 75 80
Leu Ile Pro Phe Ile Phe Thr Lys Trp Leu Gln Asp Val Phe Asn Val
85 90 95
Pro Leu Val Ile Gln Met Thr Asp Asp Glu Lys Tyr Leu Trp Lys Asp
100 105 110

Leu Thr Leu Asp Gln Ala Tyr Gly Asp Ala Val Glu Asn Ala Lys Asp
115 120 125
Ile Ile Ala Cys Gly Phe Asp Ile Asn Lys Thr Phe Ile Phe Ser Asp
130 135 140
Leu Asp Tyr Met Gly Met Ser Ser Gly Phe Tyr Lys Asn Val Val Lys
145 150 155 160
Ile Gln Lys His Val Thr Phe Asn Gln Val Lys Gly Ile Phe Gly Phe
165 170 175
Thr Asp Ser Asp Cys Ile Gly Lys Ile Ser Phe Pro Ala Ile Gln Ala
180 185 190
Ala Pro Ser Phe Ser Asn Ser Phe Pro Gln Ile Phe Arg Asp Arg Thr
195 200 205
Asp Ile Gln Cys Leu Ile Pro Cys Ala Ile Asp Gln Asp Pro Tyr Phe
210 215 220
Arg Met Thr Arg Asp Val Ala Pro Arg Ile Gly Tyr Pro Lys Pro Ala
225 230 235 240
Leu Leu His Ser Thr Phe Phe Pro Ala Leu Gln Gly Ala Gln Thr Lys
245 250 255
Met Ser Ala Ser Asp Pro Asn Ser Ser Ile Phe Leu Thr Asp Thr Ala
260 265 270
Lys Gln Ile Lys Thr Lys Val Asn Lys His Ala Phe Ser Gly Gly Arg
275 280 285
Asp Thr Ile Glu Glu His Arg Gln Phe Gly Gly Asn Cys Asp Val Asp
290 295 300
Val Ser Phe Met Tyr Leu Thr Phe Phe Leu Glu Asp Asp Asp Lys Leu
305 310 315 320
Glu Gln Ile Arg Lys Asp Tyr Thr Ser Gly Ala Met Leu Thr Gly Glu
325 330 335
Leu Lys Lys Ala Leu Ile Glu Val Leu Gln Pro Leu Ile Ala Glu His
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Thr Pro Arg Lys Leu Ser Phe Asp Phe Gln
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Pro Trp Thr Val Gln Thr Ser Ser Ala Lys Gly Ile Asp Tyr Asp Lys
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35 40 45
Arg Ile Glu Arg Ala Thr Gly Gln Arg Pro His His Phe Leu Arg Arg
50 55 60
Gly Ile Phe Phe Ser His Arg Asp Met Asn Gln Val Leu Asp Ala Tyr
65 70 75 80
Glu Asn Lys Lys Pro Phe Tyr Leu Tyr Thr Gly Arg Gly Pro Ser Ser
85 90 95
Glu Ala Met His Val Gly His Leu Ile Pro Phe Ile Phe Thr Lys Trp

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                100                 105                 110
Leu Gln Asp Val Phe Asn Val Pro Leu Val Ile Gln Met Thr Asp Asp
        115                 120                 125
Glu Lys Tyr Leu Trp Lys Asp Leu Thr Leu Asp Gln Ala Tyr Gly Asp
    130                 135                 140
Ala Val Glu Asn Ala Lys Asp Ile Ile Ala Cys Gly Phe Asp Ile Asn
145                 150                 155                 160
Lys Thr Phe Ile Phe Ser Asp Leu Asp Tyr Met Gly Met Ser Ser Gly
                165                 170                 175
Phe Tyr Lys Asn Val Val Lys Ile Gln Lys His Val Thr Phe Asn Gln
            180                 185                 190
Val Lys Gly Ile Phe Gly Phe Thr Asp Ser Asp Cys Ile Gly Lys Ile
        195                 200                 205
Ser Phe Pro Ala Ile Gln Ala Ala Pro Ser Phe Ser Asn Ser Phe Pro
    210                 215                 220
Gln Ile Phe Arg Asp Arg Thr Asp Ile Gln Cys Leu Ile Pro Cys Ala
225                 230                 235                 240
Ile Asp Gln Asp Pro Tyr Phe Arg Met Thr Arg Asp Val Ala Pro Arg
                245                 250                 255
Ile Gly Tyr Pro Lys Pro Ala Leu Leu His Ser Thr Phe Phe Pro Ala
            260                 265                 270
Leu Gln Gly Ala Gln Thr Lys Met Ser Ala Ser Asp Pro Asn Ser Ser
        275                 280                 285
Ile Phe Leu Thr Asp Thr Ala Lys Gln Ile Lys Thr Lys Val Asn Lys
    290                 295                 300
His Ala Phe Ser Gly Gly Arg Asp Thr Ile Glu Glu His Arg Gln Phe
305                 310                 315                 320
Gly Gly Asn Cys Asp Val Asp Val Ser Phe Met Tyr Leu Thr Phe Phe
                325                 330                 335
Leu Glu Asp Asp Asp Lys Leu Glu Gln Ile Arg Lys Asp Tyr Thr Ser
            340                 345                 350
Gly Ala Met Leu Thr Gly Glu Leu Lys Lys Ala Leu Ile Glu Val Leu
        355                 360                 365
Gln Pro Leu Ile Ala Glu His Gln Ala Arg Arg Lys Glu Val Thr Asp
    370                 375                 380
Glu Ile Val Lys Glu Phe Met Thr Pro Arg Lys Leu Ser Phe Asp Phe
385                 390                 395                 400
Gln
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